

**SEQUENCE LISTING**

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<120> ADIPOCYTE COMPLEMENT RELATED PROTEIN  
HOMOLOG ZACRP5

<130> 99-10C1

<150> US 09/573,733  
<151> 2000-05-18

<150> US 60/136,292  
<151> 1999-05-27

<160> 15

<170> FastSEQ for Windows Version 4.0

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<210> 1
<211> 759
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1) . . . (759)

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<400> 1
atg gca gcc ccc gcc ctg ctg ctc cta gca ctg ctg ctg ccc gtg ggg 48
Met Ala Ala Pro Ala Leu Leu Leu Leu Ala Leu Leu Leu Leu Pro Val Gly
   1           5           10          15

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gcc tgg ccc ggg ctg ccc agg agg ccc tgt gtg cac tgc tgc cgc ccg 96  
 Ala Trp Pro Gly Leu Pro Arg Arg Pro Cys Val His Cys Cys Arg Pro  
                  20                 25                 30

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gcc tgg ccc cct gga ccc tat gcc cggtg agt gac agg gac ctg tgg 144
Ala Trp Pro Pro Gly Pro Tyr Ala Arg Val Ser Asp Arg Asp Leu Trp
          35           40           45

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agg ggg gac ctg tgg agg ggg ctg cct cga gta cgg ccc act ata aac 192
Arg Gly Asp Leu Trp Arg Gly Leu Pro Arg Val Arg Pro Thr Ile Asn
      50           55           60

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atc gaa atc ctc aaa ggt gag aag ggt gag gcc ggc gtc cga ggt cgg 240  
Ile Glu Ile Leu Lys Gly Glu Lys Gly Glu Ala Gly Val Arg Gly Arg  
65 70 75 80

gcc ggc agg agc ggg aaa gag ggg ccg cca ggc gcc cg<sub>g</sub> ggc ctg cag 288  
 Ala Gly Arg Ser Gly Lys Glu Gly Pro Pro Gly Ala Arg Gly Leu Gln  
                   85                 90                 95

```

ggc cgc aga ggc cag aag ggg cag gtg ggg ccg ccg ggc gcc gcg tgc 336
Gly Arg Arg Gly Gln Lys Gly Gln Val Gly Pro Pro Gly Ala Ala Cys
          100          105          110

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cga cgt gcc tac gcc ttc tcc gtg ggc cg<sub>g</sub> cg<sub>c</sub> gag ggc ctg cac 384  
 Arg Arg Ala Tyr Ala Ala Phe Ser Val Gly Arg Arg Glu Gly Leu His  
           115              120              125

```

agc tcc gac cac ttc cag gcg gtg ccc ttc gac acg gag ctg gtg aac 432
Ser Ser Asp His Phe Gln Ala Val Pro Phe Asp Thr Glu Leu Val Asn
          130           135           140

```

ctg gac ggc gcc ttc gac ctg gcc ggc cgc ttc ctc tgc acg gtg	480
Leu Asp Gly Ala Phe Asp Leu Ala Ala Gly Arg Phe Leu Cys Thr Val	
145 150 155 160	
ccc ggc gtc tac ttc ctc agc ctc aac gtg cac acc tgg aac tac aag	528
Pro Gly Val Tyr Phe Leu Ser Leu Asn Val His Thr Trp Asn Tyr Lys	
165 170 175	
gag acc tac ctg cac atc atg ctg aac cgg cgg ccc gcg gcc gtg ctc	576
Glu Thr Tyr Leu His Ile Met Leu Asn Arg Arg Pro Ala Ala Val Leu	
180 185 190	
tac gcg cag ccc agc gag cgc agc gtc atg cag gcc cag agc ctg atg	624
Tyr Ala Gln Pro Ser Glu Arg Ser Val Met Gln Ala Gln Ser Leu Met	
195 200 205	
ctg ctg ctg gcg ggc gac gcc gtc tgg gtg cgc atg ttc cag cgc	672
Leu Leu Leu Ala Ala Gly Asp Ala Val Trp Val Arg Met Phe Gln Arg	
210 215 220	
gac cgg gac aac gcc atc tac ggc gag cac gga gac ctc tac atc acc	720
Asp Arg Asp Asn Ala Ile Tyr Gly Glu His Gly Asp Leu Tyr Ile Thr	
225 230 235 240	
ttc agc ggc cac ctg gtc aag ccg gcc gag ctg tag	759
Phe Ser Gly His Leu Val Lys Pro Ala Ala Glu Leu *	
245 250	

<210> 2  
<211> 252  
<212> PRT  
<213> Homo sapiens

<400> 2	
Met Ala Ala Pro Ala Leu Leu Leu Ala Leu Leu Pro Val Gly	
1 5 10 15	
Ala Trp Pro Gly Leu Pro Arg Arg Pro Cys Val His Cys Cys Arg Pro	
20 25 30	
Ala Trp Pro Pro Gly Pro Tyr Ala Arg Val Ser Asp Arg Asp Leu Trp	
35 40 45	
Arg Gly Asp Leu Trp Arg Gly Leu Pro Arg Val Arg Pro Thr Ile Asn	
50 55 60	
Ile Glu Ile Leu Lys Gly Glu Lys Gly Glu Ala Gly Val Arg Gly Arg	
65 70 75 80	
Ala Gly Arg Ser Gly Lys Glu Gly Pro Pro Gly Ala Arg Gly Leu Gln	
85 90 95	
Gly Arg Arg Gly Gln Lys Gly Gln Val Gly Pro Pro Gly Ala Ala Cys	
100 105 110	
Arg Arg Ala Tyr Ala Ala Phe Ser Val Gly Arg Arg Glu Gly Leu His	
115 120 125	
Ser Ser Asp His Phe Gln Ala Val Pro Phe Asp Thr Glu Leu Val Asn	
130 135 140	
Leu Asp Gly Ala Phe Asp Leu Ala Ala Gly Arg Phe Leu Cys Thr Val	
145 150 155 160	
Pro Gly Val Tyr Phe Leu Ser Leu Asn Val His Thr Trp Asn Tyr Lys	
165 170 175	
Glu Thr Tyr Leu His Ile Met Leu Asn Arg Arg Pro Ala Ala Val Leu	
180 185 190	
Tyr Ala Gln Pro Ser Glu Arg Ser Val Met Gln Ala Gln Ser Leu Met	
195 200 205	
Leu Leu Leu Ala Ala Gly Asp Ala Val Trp Val Arg Met Phe Gln Arg	
210 215 220	
Asp Arg Asp Asn Ala Ile Tyr Gly Glu His Gly Asp Leu Tyr Ile Thr	
225 230 235 240	

Phe Ser Gly His Leu Val Lys Pro Ala Ala Glu Leu  
 245 250

<210> 3

<211> 281

<212> PRT

<213> Homo sapiens

<400> 3

Met	Gly	Ser	Arg	Gly	Gln	Gly	Leu	Leu	Leu	Ala	Tyr	Cys	Leu	Leu	Leu
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Ala	Phe	Ala	Ser	Gly	Leu	Val	Leu	Ser	Arg	Val	Pro	His	Val	Gln	Gly
															30
20									25						
Glu	Gln	Gln	Glu	Trp	Gly	Thr	Glu	Glu	Leu	Pro	Ser	Pro	Pro	Asp	
															45
35									40						
His	Ala	Glu	Arg	Ala	Glu	Glu	Gln	His	Glu	Lys	Tyr	Arg	Pro	Ser	Gln
									55						60
50															
Asp	Gln	Gly	Leu	Pro	Ala	Ser	Arg	Cys	Leu	Arg	Cys	Cys	Asp	Pro	Gly
65										75					80
Thr	Ser	Met	Tyr	Pro	Ala	Thr	Ala	Val	Pro	Gln	Ile	Asn	Ile	Thr	Ile
															95
85									90						
Leu	Lys	Gly	Glu	Lys	Gly	Asp	Arg	Gly	Asp	Arg	Gly	Leu	Gln	Gly	Lys
									100						110
100										105					
Tyr	Gly	Lys	Thr	Gly	Ser	Ala	Gly	Ala	Arg	Gly	His	Thr	Gly	Pro	Lys
										115					125
115											120				
Gly	Gln	Lys	Gly	Ser	Met	Gly	Ala	Pro	Gly	Glu	Arg	Cys	Lys	Ser	His
										130					140
130											135				
Tyr	Ala	Ala	Phe	Ser	Val	Gly	Arg	Lys	Lys	Pro	Met	His	Ser	Asn	His
145											150				160
Tyr	Tyr	Gln	Thr	Val	Ile	Phe	Asp	Thr	Glu	Phe	Val	Asn	Leu	Tyr	Asp
											165				175
165												170			
His	Phe	Asn	Met	Phe	Thr	Gly	Lys	Phe	Tyr	Cys	Tyr	Val	Pro	Gly	Leu
										180					190
180											185				
Tyr	Phe	Phe	Ser	Leu	Asn	Val	His	Thr	Trp	Asn	Gln	Lys	Glu	Thr	Tyr
										195					205
195											200				
Leu	His	Ile	Met	Lys	Asn	Glu	Glu	Val	Val	Ile	Leu	Phe	Ala	Gln	
										210					220
210											215				
Val	Gly	Asp	Arg	Ser	Ile	Met	Gln	Ser	Gln	Ser	Leu	Met	Leu	Glu	Leu
225										225					240
225											230				
Arg	Glu	Gln	Asp	Gln	Val	Trp	Val	Arg	Leu	Tyr	Lys	Gly	Glu	Arg	Glu
										245					255
245											250				
Asn	Ala	Ile	Phe	Ser	Glu	Glu	Leu	Asp	Thr	Tyr	Ile	Thr	Phe	Ser	Gly
									260						270
260											265				
Tyr	Leu	Val	Lys	His	Ala	Thr	Glu	Pro							
									275						280

<210> 4

<211> 244

<212> PRT

<213> Homo sapiens

<400> 4

Met	Leu	Leu	Leu	Gly	Ala	Val	Leu	Leu	Leu	Leu	Ala	Leu	Pro	Gly	His
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Asp	Gln	Glu	Thr	Thr	Thr	Gln	Gly	Pro	Gly	Val	Leu	Leu	Pro	Leu	Pro
															30
20										25					
Lys	Gly	Ala	Cys	Thr	Gly	Trp	Met	Ala	Gly	Ile	Pro	Gly	His	Pro	Gly
										35					45
35											40				
His	Asn	Gly	Ala	Pro	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Thr	Pro	Gly	Glu
										50					60
50											55				
Lys	Gly	Glu	Lys	Gly	Asp	Pro	Gly	Leu	Ile	Gly	Pro	Lys	Gly	Asp	Ile
										65					80
65											70				
Gly	Glu	Thr	Gly	Val	Pro	Gly	Ala	Glu	Gly	Pro	Arg	Gly	Phe	Pro	Gly
										85					95
85											90				

Ile Gln Gly Arg Lys Gly Glu Pro Gly Glu Gly Ala Tyr Val Tyr Arg  
           100                 105                 110  
 Ser Ala Phe Ser Val Gly Leu Glu Thr Tyr Val Thr Ile Pro Asn Met  
           115                 120                 125  
 Pro Ile Arg Phe Thr Lys Ile Phe Tyr Asn Gln Gln Asn His Tyr Asp  
           130                 135                 140  
 Gly Ser Thr Gly Lys Phe His Cys Asn Ile Pro Gly Leu Tyr Tyr Phe  
           145                 150                 155                 160  
 Ala Tyr His Ile Thr Val Tyr Met Lys Asp Val Lys Val Ser Leu Phe  
           165                 170                 175  
 Lys Lys Asp Lys Ala Met Leu Phe Thr Tyr Asp Gln Tyr Gln Glu Asn  
           180                 185                 190  
 Asn Val Asp Gln Ala Ser Gly Ser Val Leu Leu His Leu Glu Val Gly  
           195                 200                 205  
 Asp Gln Val Trp Leu Gln Val Tyr Gly Glu Gly Glu Arg Asn Gly Leu  
           210                 215                 220  
 Tyr Ala Asp Asn Asp Asn Asp Ser Thr Phe Thr Gly Phe Leu Leu Tyr  
           225                 230                 235                 240  
 His Asp Thr Asn

<210> 5  
<211> 243  
<212> PRT  
<213> Homo sapiens

<400> 5  
 Met Arg Pro Leu Leu Val Leu Leu Leu Gly Leu Ala Ala Gly Ser  
     1                  5                 10                 15  
 Pro Pro Leu Asp Asp Asn Lys Ile Pro Ser Leu Cys Pro Gly His Pro  
     20                 25                 30  
 Gly Leu Pro Gly Thr Pro Gly His His Gly Ser Gln Gly Leu Pro Gly  
     35                 40                 45  
 Arg Asp Gly Arg Asp Gly Arg Asp Gly Ala Pro Gly Ala Pro Gly Glu  
     50                 55                 60  
 Lys Gly Glu Gly Gly Arg Pro Gly Leu Pro Gly Pro Arg Gly Asp Pro  
     65                 70                 75                 80  
 Gly Pro Arg Gly Glu Ala Gly Pro Ala Gly Pro Thr Gly Pro Ala Gly  
     85                 90                 95  
 Glu Cys Ser Val Pro Pro Arg Ser Ala Phe Ser Ala Lys Arg Ser Glu  
     100                105                110  
 Ser Arg Val Pro Pro Pro Ser Asp Ala Pro Leu Pro Phe Asp Arg Val  
     115                120                125  
 Leu Val Asn Glu Gln Gly His Tyr Asp Ala Val Thr Gly Lys Phe Thr  
     130                135                140  
 Cys Gln Val Pro Gly Val Tyr Tyr Phe Ala Val His Ala Thr Val Tyr  
     145                150                155                 160  
 Arg Ala Ser Leu Gln Phe Asp Leu Val Lys Asn Gly Glu Ser Ile Ala  
     165                170                175  
 Ser Phe Phe Gln Phe Phe Gly Gly Trp Pro Lys Pro Ala Ser Leu Ser  
     180                185                190  
 Gly Gly Ala Met Val Arg Leu Glu Pro Glu Asp Gln Val Trp Val Gln  
     195                200                205  
 Val Gly Val Gly Asp Tyr Ile Gly Ile Tyr Ala Ser Ile Lys Thr Asp  
     210                215                220  
 Ser Thr Phe Ser Gly Phe Leu Val Tyr Ser Asp Trp His Ser Ser Pro  
     225                230                235                 240  
 Val Phe Ala

<210> 6  
<211> 245  
<212> PRT  
<213> Homo sapiens

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<400> 6
Met Asp Val Gly Pro Ser Ser Leu Pro His Leu Gly Leu Lys Leu Leu
      5          10          15
Leu Leu Leu Leu Leu Leu Ala Leu Arg Gly Gln Ala Asn Thr Gly Cys
      20          25          30
Tyr Gly Ile Pro Gly Met Pro Gly Leu Pro Gly Ala Pro Gly Lys Asp
      35          40          45
Gly Tyr Asp Gly Leu Pro Gly Pro Lys Gly Glu Pro Gly Ile Pro Ala
      50          55          60
Ile Pro Gly Ile Arg Gly Pro Lys Gly Gln Lys Gly Glu Pro Gly Leu
      65          70          75          80
Pro Gly His Pro Gly Lys Asn Gly Pro Met Gly Pro Pro Gly Met Pro
      85          90          95
Gly Val Pro Gly Pro Met Gly Ile Pro Gly Glu Pro Gly Glu Glu Gly
      100         105         110
Arg Tyr Lys Gln Lys Phe Gln Ser Val Phe Thr Val Thr Arg Gln Thr
      115         120         125
His Gln Pro Pro Ala Pro Asn Ser Leu Ile Arg Phe Asn Ala Val Leu
      130         135         140
Thr Asn Pro Gln Gly Asp Tyr Asp Thr Ser Thr Gly Lys Phe Thr Cys
      145         150         155         160
Lys Val Pro Gly Leu Tyr Tyr Phe Val Tyr His Ala Ser His Thr Ala
      165         170         175
Asn Leu Cys Val Leu Leu Tyr Arg Ser Gly Val Lys Val Val Thr Phe
      180         185         190
Cys Gly His Thr Ser Lys Thr Asn Gln Val Asn Ser Gly Gly Val Leu
      195         200         205
Leu Arg Leu Gln Val Gly Glu Glu Val Trp Leu Ala Val Asn Asp Tyr
      210         215         220
Tyr Asp Met Val Gly Ile Gln Gly Ser Asp Ser Val Phe Ser Gly Phe
      225         230         235         240
Leu Leu Phe Pro Asp
      245

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<210> 7
<211> 1421
<212> DNA
<213> Homo sapiens

<220>
<221> exon
<222> (1)...(208)
<223> Zacrp5 exon 1

<221> intron
<222> (209)...(870)
<223> Zacrp5 intron 1

<221> exon
<222> (871)...(1421)
<223> Zacrp5 exon 2
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ctgcccagga gcccctgtgt gcactgtgc cggccggcct ggccccctgg accctatgcc 120
cggttgagtg acaggacact gtggaggggg gacctgtgga gggggctgcc tcgagttacgg 180
cccaactataa acatcgaaat cctcaaaggt gaggccctgt ggtgtctgcct gcatgtcccc 240
ccaccaggac ccaacagccc acaggaggatg gggagcacct ggggcttggg aggaggggcg 300
ggaggggcacc tctgagcacc agtgtctgg ctggcagcgc tccctgcaca gggaccctgt 360
ggctcccccc gcaaggcagga agaaggctgg ctgggggagg gaccatgaa ccaaagtggg 420
gtgctgagga tctctggggaa gggggccagg gttcctgaga tccccaaagt agcagccct 480
tggaaaggga gcctggcag cccgcgttgc ctgagacccc ttgacacggc tgccgtgtcc 540
cgaagctgtta ctaaggatgt gcttgggtag gaccttccca gccttctcat tctttAACAC 600
ccaacgcaga cctgtactgg ccctgaccac ccatgtcccc accctctcggtggggacggc 660

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cttgccacag gccttggctc agccacacact ttggagaacg gcttctcccc atcttacaga 720  
 cgtggacgcg gagactggga gagggggccgt cacttgaaa gagtgtgtcc ttacagtgc 780  
 cctttagcccc cagccccctgg cctgggtgct ggaatggggg aggccctgccc agcccggccc 840  
 cgaccggctgg cttdcggttt tccccctgcag gtgagaaggg tgaggccggc gtccgaggtc 900  
 gggccggcag gagcgggaaa gagggggccgc caggcgccccg gggcctgcag ggccgcagag 960  
 gccagaaggg gcaggtgggg ccgcggggcg ccgcgtgccc acgtgcctac gccgccttct  
 1020  
 ccgtggggccg ggcgcgaggc ctgcacagct ccgaccactt ccaggcggtg cccttcgaca  
 1080  
 cgagactgggt gaacctggac ggcgccttcg acctggccgc gggccgcttc ctctgcacgg  
 1140  
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 1200  
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 1260  
 gcgtcatgca ggcccagagc ctgatgctgc tgctggccgc gggcgacgccc gtctgggtgc  
 1320  
 gcatgttcca ggcgcgaccgg gacaacgcca tctacggcga gcacggagac ctctacatca  
 1380  
 ctttcagccgg ccacctggtc aagccggccg ccgagctgta g  
 1421

&lt;210&gt; 8

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; C1q aromatic motif

&lt;221&gt; VARIANT

&lt;222&gt; (2)...(6)

&lt;223&gt; Each Xaa is independently any amino acid residue

&lt;221&gt; VARIANT

&lt;222&gt; (7)...(7)

&lt;223&gt; Xaa is asparagine or aspartic acid

&lt;221&gt; VARIANT

&lt;222&gt; (8)...(11)

&lt;223&gt; Each Xaa is independently any amino acid residue

&lt;221&gt; VARIANT

&lt;222&gt; (12)...(12)

&lt;223&gt; Xaa is phenylalanine, tyrosine, trhytophan or leucine

&lt;221&gt; VARIANT

&lt;222&gt; (13)...(18)

&lt;223&gt; Each Xaa is independently any amino acid residue

&lt;221&gt; VARIANT

&lt;222&gt; (20)...(24)

&lt;223&gt; Each Xaa is independently any amino acid residue

&lt;221&gt; VARIANT

&lt;222&gt; (26)...(26)

&lt;223&gt; Xaa is any amino acid residue

&lt;221&gt; VARIANT

&lt;222&gt; (28)...(28)

&lt;223&gt; Xaa is any amino acid residue

&lt;221&gt; VARIANT

&lt;222&gt; (30)...(30)

&lt;223&gt; Xaa is any amino acid residue

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<221> VARIANT
<222> (31)...(31)
<223> Xaa is phenylalanine or tryrosine

<400> 8
Phe Xaa Xaa
  1           5           10          15
Xaa Xaa Phe Xaa Xaa Xaa Xaa Gly Xaa Tyr Xaa Phe Xaa Xaa
  20          25          30

<210> 9
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Degenerate oligonucleotide primer

<221> variation
<222> (1)...(17)
<223> Each N is independently A, T, G or C

<400> 9
msnggnntnt aytwytt                                17

<210> 10
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Degenerate oligonucleotide sequence

<221> variation
<222> (1)...(17)
<223> Each N is independently A, T, G or C

<400> 10
srnganvvng tntggbt                                17

<210> 11
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Degenerate oligonucleotide primer

<221> variation
<222> (1)...(17)
<223> Each N is independently A, T, G or C

<400> 11
rynttywsng gnywytt                                17

<210> 12
<211> 756
<212> DNA
<213> Artificial Sequence

<220>
<223> Degenerate nucleotide sequence encoding the
      polypeptide of SEQ ID NO:2

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<221> variation  
 <222> (1)...(756)  
 <223> Each N is independently T, A, G or C

<400> 12  
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 ytnccnmgnm gnccntgygt ncaytgytgy mgnccngcnt ggcncncngg ncctaygcn 120  
 mgngtnwsng aymngayyt ntggmnggn gayytnntggm gnggnytncc nmngtnmgn 180  
 ccnacnatha ayathgarat hytnaarggn garaarggng argcnggngt nmngggnmgn 240  
 gcnggnmgnw snggnaarga rggncnccn gngcnmgng gnytncargg nmgnmgnngn 300  
 caraarggnc argtnggncc nccngngcn gcntgymgnm gngcntaygc nccttywsn 360  
 gtnggnmgnm gngarggnyt ncaywsnwsn gaycayttc argcngtncc nttygayacn 420  
 garytngtta ayytngaygg nccttygay ytngcngcng gnmgnattytt ntgyacngtn 480  
 ccngngntnt ayttyytnws nytnaaygtn cayacntgga aytayaarga racntayytn 540  
 cayathatgy tnaaymgnmg nccngcngcn gtntayg cncarccnws ngarmgnwsn 600  
 gtnatgcarg cncarwsnyt natgytnytn ytngcngcng gngaygcngt ntgggtmgn 660  
 atgtycarm gngaymgnga yaaygcnath tayggngarc ayggngayyt ntayathacn 720  
 ttywsngnc ayytngtnaa rccngcngcn garytn 756

<210> 13  
 <211> 12  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Representative contig

<400> 13  
 atggcttagc tt 12

<210> 14  
 <211> 12  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Representative contig

<400> 14  
 tagcttgagt ct 12

<210> 15  
 <211> 12  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Representative contig

<400> 15  
 agccatcagc tg 12